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| (54) Title: PROTEIN TYROSINE KINASE 2 (PYK2), N (57) Abstract  This invention is directed to nucleic acids encoding protein using the nucleic acids, and to assays for inhibitors  | proteir   | tyrosine kinase 2 (PYK2), to murine PYK2, to methods of making this |
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TITLE OF THE INVENTION
PROTEIN TYROSINE KINASE 2 (PYK2), NUCLEIC ACIDS, AND
ASSAY

## 5 BRIEF DESCRIPTION OF THE INVENTION

This invention is directed to nucleic acids encoding protein tyrosine kinase 2 (PYK2), to murine PYK2, to methods of making this protein using the nucleic acids, and to assays for inhibitors of PYK2.

#### 10 BACKGROUND OF THE INVENTION

Protein tyrosine kinase 2 (PYK2), also known as Cell Adhesion Kinase β (CAKβ) and Related Adhesion Focal Tyrosine Kinase (RAFTK) is a recently described member of the focal adhesion kinase family (Avraham et al., 1995 J. Biol. Chem. 270:27742-27751; Lev et al., 15 1995 Nature. 376:737-745; and Sasaki, et al., 1995 J. Biol. Chem. 270:21206-21219.). PYK2 was first cloned from human brain as a Grb-2 binding protein, and has also been cloned from rat and human brain libraries. There have been conflicting reports as to its cellular expression. In one study, abundant PYK2 transcripts were found in brain and lower levels were detected in the kidney. In another report, 20 PYK2 expression was also found to be most abundant in rat brain, but its transcripts could also be detected in kidney, spleen, lung, intestine and epididymis. PYK2 transcripts were also detected in rat fibroblast 3Y1 and WFB cell lines, as well as in the human T cell leukemia Jurkat line. 25 When cloned from the human megakaryocytic CMK cell line and from mouse brain, it was found to have wider tissue distribution beyond brain, notably spleen, lung, thymus and peripheral blood leukocytes. In addition, expression of PYK2 was reported in human CD34+ marrow cells, megakaryocytes and platelets.

#### DETAILED DESCRIPTION OF THE INVENTION

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One aspect of this invention is are nucleic acids, substantially free from associated nucleic acids, which encode murine protein tryosine kinase 2 (PYK2). In one embodiment, the nucleic acid which encodes PYK2 is a DNA.

Another aspect of this invention is murine PYK2 cDNA, Murine PYK2 DNA is set forth in Figure 1 (SEQ ID NO:5).

Yet another aspect of this invention is murine PYK2 which is free from associated murine proteins. One murine PYK2 is set forth in Figure 1 (SEQ ID NO:6).

Another aspect of this invention is a method of making PYK2 by introducing nucleic acids into a cell, the nucleic acids comprising nucleic acids which encode PYK2, under conditions which transcription and translation of PYK2 occur. It is preferred that the nucleic acids be present in a vector, such as a plasmid or baculovirus vector. It is also preferred that the nucleic acids be under the control of transcriptional control elements, such as promoters and optionally enhancers. Such control elements are well known in the art.

Host cells which express PYK2 are also part of this invention. Preferred host cells include mammalian cells, insect cells, yeast and bacterial cells such as *E. coli*. Cell lines which permanently (rather than transiently) express murine PYK2 are also another aspect of this invention.

The recombinant PYK2, which is made using the cloning process of this invention may be used in assays in order to further characterize the biological function of PYK2 and to identify compounds such as agonists and antagonists which modulate its activity. A further aspect of this invention is an assay for the identification of compounds which modulate the activity of PYK2, and particularly inhibitors of PYK2 activity. This assay comprises the steps of: contacting recombinant PYK2 with a tyrosine substrate in the presence of radiolabeled ATP and a putative activity-modifying compound, and measuring the amount of radiolabeled tyrosine which is formed; and optionally comparing the amount of radiolabeled tyrosine formed in the

presence of the putative activity-modifying compound with that formed in the absence of the putative activity-modifying compound.

Integrins are the major family of cell surface receptors that mediate adhesive interactions, either to adjacent cells or to the extracellular matrix. Integrin signalling is mediated through the focal adhesion kinase (FAK) family of proteins. PYK2 is a member of the FAK family, and is involved in integrin-mediated signal transduction pathways in megakaryocytes, brain tissue and hematopoietic cells. Modulators of PYK2 would therefore be potential therapeutic agents for modulating platelet levels.

#### BRIEF DESCRIPTION OF THE FIGURES

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Figure 1 is the cDNA sequence of mouse PYK2 and the deduced protein sequence. Intron sequences are in lower case letters. The exon sequence is capitalized. The boxed sequence of the deduced protein indicates the kinase domain. The circled prolines of the deduced protein indicate the proline rich domain.

As used throughout the specification and claims, the following definitions apply:

"PYK2" means protein tyrosine kinase 2, allelic variations of protein tyrosine kinase 2, and mutations or fragments thereof which retain at least about 85%, and preferably at least about 90% of the biological activity of native PYK2.

"Native PYK2" means the protein tyrosine kinase which is naturally occuring in an organism.

"Substantially free from associated nucleic acids" means that in a sample, there is less than about 5% (by weight) nucleic acids present which are other than nucleic acids encoding PYK2.

"Substantially free from associated murine proteins" means that in a sample, there is less than about 5% (by weight) protein which is other than murine PYK2.

"FAK" means focal adhesion kinase.

"Heterologous" PYK2 nucleic acid means that the nucleic acid was introduced to the cell, without regard as to whether the nucleic acid is from the same species as the cell; alternatively it refers to nucleic

acids encoding PYK2 in a cell whose ancestor had PYK2 introduced into the cell.

"Heterologous" PYK2 protein means that the PYK2 was encoded by a heterologous nucleic acid.

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FAK proteins, which are involved in cell adhesion processes, were not detected in a number of macrophage cell lines and it was therefore hypothesized that another cell adhesion-dependent kinase, homologous to FAK, may assume its function in these cells. PYK2 was recently identified as another member of the FAK family and its expression was detected in spleen, thymus, lung and peripheral blood leukocytes (Avraham, et al., 1995 supra; Sasaki, et al., 1995 supra). To evaluate PYK2 as a possible adhesion-dependent kinase in macrophages, specific probes were generated for PYK2 and FAK which were used to examine the expression of PYK2 and FAK in mouse tissues. As previously reported, for other species, PYK2 is highly expressed in brain and spleen, and at lower levels in kidney, lung and liver and has a more restricted tissue distribution than FAK.

Using a PYK2 probe, the full length cDNA was cloned from a mouse spleen cDNA library. The deduced amino acid sequence of the full length clone was found to be identical to the recently published amino acid sequence of the mouse RAFTK (Avraham, et al., 1995, supra).

In addition, the full length FAK was cloned from a mouse osteoblastic MB1.8 cell line (Wesolowski, et al., 1995, Exp. Cell Res., 219: 679-686.).

PYK2 and FAK cDNAs were subsequently transfected into human embryonic kidney (HEK) 293 cells. Cell lines which permanently express either PYK2 or FAK were established and the expression levels of the exogeneously expressed mouse kinases were assessed by northern analysis.

The following Examples are presented to better illustrate the invention.

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**EXAMPLE 1** 

#### Cell Culture

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Macrophages were induced by thioglycolate injection into the peritoneal cavities of adult BALB/c mice. After 4 days, cells were collected, washed and cultured in RPMI 1640 medium containing 10% FBS. After 3h at 37°C, the cultures were washed extensively to remove non-adherent cells and cultured overnight before samples were prepared for immunoprecipitation. Bone marrow derived macrophages were prepared as described by Li and Chen, 1995 J. Leuk. Biol. 57:484-490, which is hereby incorporated by reference. Non adherent cells were cultured in RPMI completed medium in the presence of human macrophage colony-stimulating factor (MCS-F, 250 units/ml, Genetics Institute, Cambridge, MA). Differentiated macrophages were prepared for immunoprecipitation after 5 days in culture.

Bone marrow derived osteoclast-like cells were prepared as described by Wesolowski, et al., 1995 Exp. Cell Res. 219:679-686, which is hereby incorporated by reference. After collagenase-dispase treatment, mononucleated tartrate resistant phosphatase positive cells were released from the tissue culture plate using 30 nM echistatin (Merck Res. Labs., West Point, PA). Freshly isolated osteoclast-like cells were immediately solubilized in immunoprecipitation buffer.

#### **EXAMPLE 2**

## 25 cDNA Cloning and Expression of mouse PYK2

Specific probes for mouse PYK2 and FAK were initially generated based on the non-homologous region between the proteins, which is adjacent to the C-terminal of the kinase domain. Using polymerase chain reaction (PCR), a specific probe for PYK2 (570bp) was generated using the 5'-primer AGTGA CATTT ATCAG ATGGA G (SEQ. ID. NO:1) and the 3'-primer GAATG GACTG TGCAC CGAGC C (SEQ. ID. NO:2) with cDNAs of mouse bone marrow derived osteoclast-like cells as template (Wesolowski, et al., 1995, supra).

Similarly, a specific probe for FAK (700bp) was generated using the following primers: 5'- CAGCA CACAA TCCTG GAGGA G

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(SEQ. ID. NO:3) and 3'- GCTGA AGCTT GACAC CCTCA T (SEQ. ID. NO. 4) with cDNAs of mouse osteoblastic MB1.8 cells as template (Wesolowski, et al., 1995, supra). These probes were confirmed by sequencing analysis. PYK2 cDNA fragments were cloned from a mouse spleen λ-ZAP II cDNA library (Stratagene, La Jolla, CA) using the specific PYK2 probe. Full length PYK2 cDNA were constructed by ligation of two overlapping clones at the VspI site. The amino acid sequence of the isolated PYK2 cDNA clone was identical to the previously published mouse RAFTK sequence (Avraham, et al., 1995 supra). Full length FAK cDNA was generated by PCR according to the published sequence as described in Hanks, et al., 1992 Proc. Natl. Acad. Sci. USA. 89:8487-8491.

Both PYK2 and FAK cDNAs were subcloned into pCDNA3 plasmid (InVitrogen, San Diego, CA) and transfected into human embryonic kidney (HEK) 293 cells (ATCC, Rockland, MD) by electroporation at 200V, 960 µF using a GenePulser (Biorad Labs, Richmond, CA). HEK 293 cells were subsequently subjected to G418 selection (800 µg/ml, Gibco BRL) and clones were picked after 3 weeks in selection medium.

Expression of PYK2 and FAK in HEK293 cells were confirmed by Northern analysis using the respective probes, and Western blots were performed using anti-PYK2 antibodies. Mouse multiple tissue Northern blot was purchased from Clonetech (Palo Alto, CA) and hybridization of the Northern blot using probes specific for PYK2, FAK and glyceraldehde 3-phosphate dehydrogenase (GAPDH) were performed as described previously (Wesolowski, et al., 1995, supra).

#### EXAMPLE 3

Production and Affinity Purification of Polyclonal Antibodies to mouse PYK2

The PYK2 C-terminal domain (from Methionine residue 685 to end) was amplified by PCR using the mouse PYK2 as template. Amplified product was cloned into plasmid pGEX-4T (Pharmacia Biotech., Piscataway, NJ) and transformed in E.coli XL1-Blue (Stratagene). Expression of GST-PYK2 C-terminal fragment was induced using 0.5 mM IPTG, purified and cleaved from GST with thrombin, essentially according to the instructions of the manufacturer (Pharmacia). The purified C-terminal fragment of mouse PYK2 was used to immunize two rabbits (Research Genetics, Huntsville, AL) and the titers of both antisera were initially determined by ELISA using the recombinant C-terminal fragment of PYK2. Specificity of the immune sera was subsequently determined by Western blot by comparison to the preimmune sera. Polyclonal antibodies were then affinity purified by passing the combined fractions of both antisera through an affinity column, which was constructed using the same purified antigen cross linked to CNBr-activated Sepharose 4B according to the instructions of the manufacturer (Pharmacia).

The antibodies were eluted from the column using 0.2 M Glycine, pH 2.5 and 1mM EGTA and the eluted fraction was then dialyzed against PBS containing 0.02% azide. Anti-PYK2 antibodies were stored at -70°C at a concentration of 0.5mg/ml.

#### **EXAMPLE 4**

#### In vitro Kinase Assay

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30 After cell attachment to ECM, IC-21 cells were solubilized in TNE lysis buffer containing 50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1% NP-40, 1mM EDTA, 10% glycerol, 50 mM NaF, 1 mM sodium vanadate and protease inhibitors as described above. PYK2 were immunoprecipitated from the clarified lysates, half of the sample was subjected to immunoblotting with anti PYK2 antibodies, as described

above, and the other half was washed 2 times with the same lysis buffer, and with kinase assay buffer (1X) containing 20 mM Tris-HCl, pH 7.4, 100 mM NaCl, 10 mM MnCl2 and 1 mM dithiothreitol. After removal of the wash buffer, 50  $\mu$ l of kinase assay buffer containing 5  $\mu$ Ci [ $\gamma$ -32P] ATP (3000 Ci/mmol, Amersham), 10 mM ATP, 0.1% BSA and 100 µg of poly (Glu, Tyr) (molar ratio 4:1; Sigma) was added to the beads and incubated for 10 min at 30°C (Howell and Cooper, 1995 Mol. Cell. Biol. 14:5402-5411). The reaction mixtures (25  $\mu$ l) were added to 25  $\mu$ l of 30% trichloroacetic acid (TCA) and 0.1 M sodium pyrophosphate, followed by incubation at 4°C for 15 min. The precipitated proteins were transferred to a Multiscreen-FC filter plate (Millipore, Marlborough, MA), washed with ice cold 15% TCA (3X), allowed to dry and incorporation of 32P into the substrate was counted on a Packard top count microplate scintillation counter (Packard, Meriden, CT). Each assay were performed as triplicate. The specific activity was determined by comparing the radioactive counts with immunoblot signals.

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#### SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: DUONG, LE T.
  RODAN, GIDEON A.
- (ii) TITLE OF THE INVENTION: PROTEIN TYROSINE KINASE 2 (PYK2), NUCLEIC ACIDS AND ASSAY
- (iii) NUMBER OF SEQUENCES: 6
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  - (B) STREET: P.O. Box 2000, 126 E. Lincoln Avenue
  - (C) CITY: Rahway
  - (D) STATE: NJ
  - (E) COUNTRY: USA
  - (F) ZIP: 07065-0900
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/037,561
  - (B) FILING DATE: 11-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sabatelli, Anthony D
  - (B) REGISTRATION NUMBER: 34,714
  - (C) REFERENCE/DOCKET NUMBER: 19792
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 732-594-1935
  - (B) TELEFAX: 732-594-4720
  - (C) TELEX:
  - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  |    |
|--|----|
| AGTGACATTT ATCAGATGGA G  | 21 |
| (2) INFORMATION FOR SEQ ID NO:2:   |    |
| <ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>   |    |
| (ii) MOLECULE TYPE: Other  |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  |    |
| GAATGGACTG TGCACCGAGC C  | 21 |
| (2) INFORMATION FOR SEQ ID NO:3:   |    |
| <ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>   |    |
| (ii) MOLECULE TYPE: Other  |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  |    |
| CAGCACACAA TCCTGGAGGA G  | 21 |
| (2) INFORMATION FOR SEQ ID NO:4:   |    |
| <ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>   |    |
| (ii) MOLECULE TYPE: Other  |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  |    |
| GCTGAAGCTT GACACCCTCA T  | 21 |
| (2) INFORMATION FOR SEQ ID NO:5:   |    |
| <ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 3981 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul> |    |
| (ii) MOLECULE TYPE: cDNA   |    |

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|            |            |            |            | CGCGTCCTAC         |            | 60   |
|------------|------------|------------|------------|--------------------|------------|------|
|            |            |            |            | GCGCCTCGCC         |            | 120  |
| CAATGTGCCG | GTCCTAGCTG | CAGTCTGAGA | GGATGTCCGG | ${\tt GGTGTCTGAG}$ | CCCTTGAGCC | 180  |
| GTGTAAAAGT | GGGCACTTTA | CGCCGGCCTG | AGGGCCCCCC | AGAGCCCATG         | GTGGTGGTAC | 240  |
| CAGTGGATGT | GGAGAAGGAA | GACGTGCGCA | TCCTCAAGGT | CTGCTTCTAC         | AGCAACAGCT | 300  |
| TCAACCCAGG | GAAGAACTTC | AAGCTTGTCA | AATGCACAGT | GCAGACAGAG         | ATCCAGGAGA | 360  |
|            |            |            |            | CATCCAGCTG         |            | 420  |
|            |            |            |            | CTGGCTGCAC         |            | 480  |
| CCGTGGGCGA | AGTGCAGGAC | AAGTATGAAT | GTCTACACGT | ${\tt GGAAGCTGAG}$ | TGGAGGTATG | 540  |
|            |            |            |            | CCTGAAAGAA         |            | 600  |
| CATTGCTGTA | CTTTTATCAA | CAGCTCCGGA | ATGACTACAT | GCAACGCTAC         | GCCAGCAAGG | 660  |
| TCAGTGAAGG | CATGGCTCTG | CAGCTGGGCT | GTCTGGAGCT | CAGGAGATTC         | TTCAAGGACA | 720  |
|            |            |            |            | CCTGGAAAAA         |            | 780  |
| TGGACCTGTT | TTTCCCAAAG | CAGATGCAGG | ААААСТТААА | GCCCAAGCAG         | TTCCGGAAGA | 840  |
| TGATCCAGCA | GACCTTCCAG | CAGTATGCAT | CACTCCGGGA | GGAAGAGTGT         | GTCATGAAAT | 900  |
| TCTTCAATAC | CCTAGCGGGC | TTTGCCAACA | TTGACCAGGA | GACCTACCGC         | TGCGAACTCA | 960  |
|            |            |            |            | TAAAGGCATC         |            | 1020 |
| CAAGTCAAGA | TACAAAGCCC | ACCTGCCTGG | CCGAGTTTAA | GCAGATCAGA         | TCCATCAGGT | 1080 |
| GCCTCCCATT | GGAAGAGACC | CAGGCAGTCC | TGCAGCTGGG | CATCGAGGGT         | GCCCCCAGT  | 1140 |
| CCTTGTCTAT | CAAAACGTCG | TCCCTGGCAG | AGGCTGAGAA | CATGGCTGAT         | CTCATAGATG | 1200 |
| GCTACTGCAG | GCTGCAAGGA | GAACATAAGG | GCTCTCTCAT | CATGCATGCC         | AAGAAAGATG | 1260 |
|            |            |            |            | CCTGGAGGCT         |            | 1320 |
| ACCTCTCAGA | AAGCTGCAGC | ATAGAGTCAG | ACATCTATGC | GGAGATTCCC         | GATGAGACCC | 1380 |
| TGCGAAGACC | AGGAGGTCCA | CAGTACGGTG | TTGCCCGTGA | AGAAGTAGTT         | CTTAACCGCA | 1440 |
| TTCTGGGTGA | AGGCTTCTTT | GGGGAGGTCT | ATGAAGGTGT | CTACACGAAC         | CACAAAGGGG | 1500 |
|            |            |            |            | TACCCAGGAC         |            | 1560 |
| AGTTCATGAG | TGAGGCAGTG | ATCATGAAGA | ATCTTGACCA | CCCTCACATC         | GTGAAGCTGA | 1620 |
| TTGGCATCAT | TGAAGAGGAA | CCCACCTGGA | TTATCATGGA | ACTGTATCCT         | TATGGGGAGC | 1680 |
|            |            |            |            | ACCCACTCTG         |            | 1740 |
| CCCTACAGAT | ATGCAAAGCC | ATGGCCTATC | TGGAGAGCAT | CAACTGTGTG         | CACAGGGATA | 1800 |
| TTGCTGTCCG | GAACATCCTG | GTGGCCTCTC | CTGAGTGTGT | GAAGCTGGGG         | GACTTTGGGC | 1860 |
| TCTCCCGGTA | CATTGAGGAC | GAAGACTATT | ACAAAGCCTC | TGTGACACGT         | CTACCCATCA | 1920 |
| AATGGATGTC | CCCCGAGTCC | ATCAACTTCC | GCCGCTTCAC | AACCGCCAGT         | GATGTCTGGA | 1980 |
| TGTTTGCTGT | ATGCATGTGG | GAGATCCTCA | GCTTTGGGAA | GCAGCCTTTC         | TTCTGGCTCG | 2040 |
| AAAATAAGGA | TGTCATCGGA | GTGCTGGAGA | AAGGGGACAG | GCTGCCCAAG         | CCCGAACTCT | 2100 |
| GTCCGCCTGT | CCTTTACACA | CTCATGACTC | GCTGCTGGGA | CTACGACCCC         | AGTGACCGGC | 2160 |
| CCCGCTTCAC | GGAGCTTGTG | TGCAGCCTCA | GTGACATTTA | TCAGATGGAG         | AAGGACATTG | 2220 |
|            |            |            |            | AATATTGGAG         |            | 2280 |
| TTCAGGAACC | CCCACCCAAG | CCCAGCCGGC | CCAAGTACAG | ACCTCCTCCA         | CAGACCAACC | 2340 |
| TGCTGGCTCC | TAAGCTGCAG | TTCCAGGTCC | CTGAGGGTCT | GTGTGCCAGC         | TCTCCTACGC | 2400 |
| TTACCAGCCC | TATGGAGTAT | CCATCTCCAG | TTAACTCGCT | GCACACCCCA         | CCTCTCCACC | 2460 |
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| GAGAAGAGGC | CCAGCAGCTC | TGGGAGGCAG | AGAAGATCAA | GATGAAGCAG         | GTCCTAGAAA | 2580 |
| GACAGCAGAA | GCAGATGGTG | GAAGATTCCC | AGTGGCTGAG | GCGAGAGGAA         | AGATGCTTGG | 2640 |
| ACCCTATGGT | TTATATGAAT | GACAAGTCCC | CACTGACTCC | AGAGAAGGAG         | GCCGGCTACA | 2700 |
| CGGAGTTCAC | AGGGCCCCCA | CAGAAACCAC | CTCGGCTCGG | TGCACAGTCC         | ATTCAGCCCA | 2760 |
| CAGCCAACCT | GGACAGGACC | GATGACCTCG | TGTACCACAA | TGTCATGACC         | CTGGTGGAGG | 2820 |
| CTGTGCTGGA | ACTCAAGAAC | AAGCTTGGCC | AGTTGCCCCC | TGAGGACTAT         | GTGGTGGTGG | 2880 |
| TGAAGAACGT | GGGGCTGAAC | CTGCGGAAGC | TCATCGGCAG | TGTGGACGAT         | CTCTTGCCCT | 2940 |
| CCTTGCCGGC | ATCTTCGAGG | ACAGAGATTG | AAGGGACCCA | GAAACTGCTC         | AACAAAGACC | 3000 |
| TGGCAGAGCT | CATCAACAAG | ATGAAGTTGG | CTCAGCAGAA | CGCCGTGACG         | TCCCTGAGTG | 3060 |
| AGGACTGCAA | GCGCCAGATG | CTCACAGCGT | CCCATACCCT | GGCTGTGGAT         | GCCAAGAACC | 3120 |
| TGCTGGATGC | TGTGGACCAA | GCCAAGGTTG | TGGCTAATCT | GGCCCACCCG         | CCTGCAGAGT | 3180 |
| GATCAAGAGA | GGGGCCACCT | GCCTGCATCT | TCTGCCCCCA | CCTGTCTTGG         | CATACCTTTC | 3240 |
|            |            |            |            |                    |            |      |

| CTGCCTTGCC TTTGGTTATT | GGTCTTCCAG | GGAAAGCTGA | GAAGAGTCCA | TCCCCCTTGC | 3300 |
|-----------------------|------------|------------|------------|------------|------|
| CACTTTGCAC GACACCCCT  | CTTCCCCCAA | CCCACCCCAG | ACTGTGCTAC | TCAGGCTGCA | 3360 |
| TCTGGACAGA AAGGACTCTG | GGCACAGACA | CGGGGTGGGG | TGACATAGTT | CATAGGGGTA | 3420 |
| CTACTGCCAG CCACTCCCTC | TTACCCCAGC | CTGGGTTGCT | GGAGCATCAT | TGGGGTCATG | 3480 |
| AGTGTACCCC TAACGGCCAA |            |            |            |            | 3540 |
| CTTCCTCTTC AGCCCTCAGG | GACCCCTGAT | ACAGAGGGGA | CAGAGAGGGG | TTTTATTTGT | 3600 |
| AGAGAAGCTG GTGAGATGAG | GGCTGGACCT | GGCTCTCTTG | TACAGTGTAC | ATTGGAATTT | 3660 |
| ATTTAATGTG AGTTTGACCT | GGATGGACAG | CCAAGGGCCA | TAGTCCAGGA | GCAAACCAAT | 3720 |
| CCAGTCACAG GACTCTGTGT | TTTATGGAAC | TGAGTGCCAC | AGGAAGAAGC | AGAGAGTCGG | 3780 |
| AGGTCAGAAT GGACTTTGTG |            |            |            |            | 3840 |
| CTTTTCTTAC GTCTCCTTTT |            |            |            |            | 3900 |
| GTCTGTGGAG AACATTTACC |            | TTGATCGGTG | GTTGAATTAA | AATTATTACC | 3960 |
| ATTTGCTTTG TGGCTCGTGC | C          |            |            |            | 3981 |

#### (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1009 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| 1          |            |            |            | 5          | Glu        |            |            |            | 10         |            |            |            |            | 15         |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg        | Arg        | Pro        | G1u<br>20  | Gly        | Pro        | Pro        | Glu        | Pro<br>25  | Met        | Val        | Val        | Val        | Pro<br>30  | Val        | Asp        |
| Val        | Glu        | Lys<br>35  | Glu        | Asp        | Val        | Arg        | Ile<br>40  | Ļeu        | Lys        | Val        | Cys        | Phe<br>45  | Tyr        | Ser        | Asn        |
| Ser        | Phe<br>50  | Asn        | Pro        | Gly        | Lys        | Asn<br>55  | Phe        | Lys        | Leu        | Val        | Lys<br>60  | Cys        | Thr        | Val        | Gln        |
| 65         |            |            |            |            | Ile<br>70  |            |            |            |            | 75         |            |            |            |            | 80         |
| Gly        | Pro        | Asn        | Ile        | Gln<br>85  | Leu        | Ala        | Glu        | Cys        | Tyr<br>90  | Gly        | Leu        | Arg        | Leu        | Lys<br>95  | His        |
|            |            |            | 100        |            | Ile        |            |            | 105        |            |            |            |            | 110        |            |            |
|            |            | 115        |            |            | Tyr        |            | 120        |            |            |            |            | 125        |            |            | _          |
| Tyr        | Asp<br>130 | Leu        | Gln        | Ile        | Arg        | Tyr<br>135 | Leu        | Pro        | Glu        | Asp        | Phe<br>140 | Met        | Glu        | Ser        | Leu        |
| Lys<br>145 | Glu        | Asp        | Arg        | Thr        | Thr<br>150 | Leu        | Leu        | Tyr        | Phe        | Tyr<br>155 | Gln        | Gln        | Leu        | Arg        | Asn<br>160 |
| Asp        | Tyr        | Met        | Gln        | Arg<br>165 | Tyr        | Ala        | Ser        | Lys        | Val<br>170 | Ser        | Glu        | Gly        | Met        | Ala<br>175 | Leu        |
| Gln        | Leu        | Gly        | Cys<br>180 | Leu        | Glu        | Leu        | Arg        | Arg<br>185 | Phe        | Phe        | Lys        | Asp        | Met<br>190 | Pro        | His        |
| Asn        | Ala        | Leu<br>195 | Asp        | Lys        | Lys        | Ser        | Asn<br>200 | Phe        | Glu        | Leu        | Leu        | Glu<br>205 | Lys        | Glu        | Val        |
|            | 210        |            |            |            | Phe        | 215        |            |            |            |            | 220        | Asn        |            |            |            |
| 225<br>25  | Gln        | Phe        | Arg        | Lys        | Met<br>230 | Ile        | Gln        | Gln        | Thr        | Phe<br>235 | Gln        | Gln        | Tyr        | Ala        | Ser<br>240 |

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Leu Arg Glu Glu Cys Val Met Lys Phe Phe Asn Thr Leu Ala Gly
               245
                                  250
Phe Ala Asn Ile Asp Gln Glu Thr Tyr Arg Cys Glu Leu Ile Gln Gly
           260
                              265
Trp Asn Ile Thr Val Asp Leu Val Ile Gly Pro Lys Gly Ile Arg Gln
                         280
                                             285
Leu Thr Ser Gln Asp Thr Lys Pro Thr Cys Leu Ala Glu Phe Lys Gln
                    295
                                          300.
Ile Arg Ser Ile Arg Cys Leu Pro Leu Glu Glu Thr Gln Ala Val Leu
                  310
                                      315
Gln Leu Gly Ile Glu Gly Ala Pro Gln Ser Leu Ser Ile Lys Thr Ser
               325
                                  330
Ser Leu Ala Glu Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys
          340
                      345
Arg Leu Gln Gly Glu His Lys Gly Ser Leu Ile Met His Ala Lys Lys
      355
                        360
Asp Gly Glu Lys Arg Asn Ser Leu Pro Gln Ile Pro Thr Leu Asn Leu
   370
                      375
                                       380
Glu Ala Arg Arg Ser His Leu Ser Glu Ser Cys Ser Ile Glu Ser Asp
                 390
                                      395
Ile Tyr Ala Glu Ile Pro Asp Glu Thr Leu Arg Arg Pro Gly Gly Pro
               405
                                  410
Gln Tyr Gly Val Ala Arg Glu Glu Val Val Leu Asn Arg Ile Leu Gly
           420
                              425
                                                 430
Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys
       435
                          440
                                              445
Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr
                      455
Gln Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn
465
                   470
                                      475
Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Glu
              485
                                  490
                                                      495
Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His
           500
                              505
Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Pro Thr Leu Val Leu
       515
                           520
                                              525
Tyr Thr Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn
                     535
                                         540
Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro
                  550
                                      555
Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp
               565
                                   570 .
Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met
                               585
                                                  590
Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val
       595
                           600
                                              605
Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln
                       615
                                           620
Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys
                  630
                                     635
Gly Asp Arg Leu Pro Lys Pro Glu Leu Cys Pro Pro Val Leu Tyr Thr
             645
                                 650
Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe
           660
                               665
Thr Glu Leu Val Cys Ser Leu Ser Asp Ile Tyr Gln Met Glu Lys Asp
                           680
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Ile Ala Ile Glu Gln Glu Arg Asn Ala Arg Tyr Arg Pro Pro Lys Ile
                    695
                                      700
Leu Glu Pro Thr Thr Phe Gln Glu Pro Pro Pro Lys Pro Ser Arg Pro
                710
                                715
Lys Tyr Arg Pro Pro Pro Gln Thr Asn Leu Leu Ala Pro Lys Leu Gln
             725
                      730 735
Phe Gln Val Pro Glu Gly Leu Cys Ala Ser Ser Pro Thr Leu Thr Ser
         740 745 750
Pro Met Glu Tyr Pro Ser Pro Val Asn Ser Leu His Thr Pro Pro Leu
      755
                       760
His Arg His Asn Val Phe Lys Arg His Ser Met Arg Glu Glu Asp Phe
                    775
                                   780
Ile Arg Pro Ser Ser Arg Glu Glu Ala Gln Gln Leu Trp Glu Ala Glu
                               795
      790
Lys Ile Lys Met Lys Gln Val Leu Glu Arg Gln Gln Lys Gln Met Val
         805
                               810
Glu Asp Ser Gln Trp Leu Arg Arg Glu Glu Arg Cys Leu Asp Pro Met 820 830
Val Tyr Met Asn Asp Lys Ser Pro Leu Thr Pro Glu Lys Glu Ala Gly
           840
                               845
Tyr Thr Glu Phe Thr Gly Pro Pro Gln Lys Pro Pro Arg Leu Gly Ala
                    855
                                     860
Gln Ser Ile Gln Pro Thr Ala Asn Leu Asp Arg Thr Asp Asp Leu Val
                 870
                                  875
Tyr His Asn Val Met Thr Leu Val Glu Ala Val Leu Glu Leu Lys Asn
            885
                              890
                                               895
Lys Leu Gly Gln Leu Pro Pro Glu Asp Tyr Val Val Val Lys Asn
         900
                          905
                                           910
Val Gly Leu Asn Leu Arg Lys Leu Ile Gly Ser Val Asp Asp Leu Leu
915 920 925
      915
                       920
                                         925
Pro Ser Leu Pro Ala Ser Ser Arg Thr Glu Ile Glu Gly Thr Gln Lys
                   935
                                     940
Leu Leu Asn Lys Asp Leu Ala Glu Leu Ile Asn Lys Met Lys Leu Ala
                950
                                  955
Gln Gln Asn Ala Val Thr Ser Leu Ser Glu Asp Cys Lys Arg Gln Met
             965
                               970
                                       975
Leu Thr Ala Ser His Thr Leu Ala Val Asp Ala Lys Asn Leu Leu Asp
                          985 990
Ala Val Asp Gln Ala Lys Val Val Ala Asn Leu Ala His Pro Pro Ala
              1000
                                1005
  1
```

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#### WHAT IS CLAIMED IS:

1. A nucleic acid, free from associated nucleic acids which encodes murine protein tyrosine kinase 2 (PYK2).

5

- 2. A nucleic acid according to Claim 1 which is DNA.
- 3. Murine PYK2 cDNA.

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- 4. Murine PYK2 cDNA which is set forth in Figure 1.
- 5. A cell line comprising heterologous PYK2, and which expresses PYK2.
- 15 6. An assay to identify compounds which alter the activity of PYK2 comprising:
  - a) contacting recombinant PYK2 with a tyrosine substrate in the presence of radiolabeled ATP and a putative activity-modifying compound;
- 20 b) measuring the amount of radiolabeled tyrosine which is formed; and
  - c) optionally comparing the amount of radiolabeled tyrosine formed in the presence of the putative activity-modifying compound with that formed in the absence of the putative activity-modifying compound.

TITLE OF THE INVENTION
PROTEIN TYROSINE KINASE 2 (PYK2), NUCLEIC ACIDS, AND ASSAY

## 5 ABSTRACT OF THE INVENTION

This invention is directed to nucleic acids encoding protein tyrosine kinase 2 (PYK2), to murine PYK2, to methods of making this protein using the nucleic acids, and to assays for inhibitors of PYK2.

| attagagacactcaacctcagcactcgaagcagagcacacactgagagacacacagacacacac  | 09       | 120  | 180           | 10 | 240  | 30  | 300        | 20  | 360       | 70 | 420  | 90       | 480  | 110 | 540  | 130 | 009  | 150 | 9    | 170            | 720  | 190      |  |
|---|----------|------|---------------|----|------|-----|------------|-----|-----------|----|------|----------|------|-----|------|-----|------|-----|------|----------------|------|----------|--|
| attegeggeegtegaectegaegteetgeagagegegetetaectgegeget<br>tgegeteacetggeceagecetgaeagagteegegeetegeegaggae<br>caatgtgeeggteetagetgeagtetgaeggetegegeetegeegaggae<br>M S G V S E P L S<br>GTGTAAAAGTGGGCACTTTACGCCGCCTGAGGGCCCCCAGAGCCCATGGTGGTGGT<br>V K V G T L R R P E G P P E P M V V V<br>CAGTGGATGTGGAAGACGTGCTGCTCTCAAGGTCTGTTCTACAGCAACAG<br>V D V E K E D V R C T V C F Y S N S<br>TCAACCCAGGGAAGACTTGTCAAATGCACAGTGCTGCTTCTACAGCAACAG<br>N D K K L V C F Y S N E C<br>TCATCACCCAGGGAAGACTTGTCAAATGCACAGATGCAGATGGATG   | )<br>Jgc | tg   | ပ္ပ           | œ  | AC   | A   | CT         | ſz, | <b>69</b> | Н  | CH   |          | GA   | EH  | ŢĞ   | Ω   | S,   | E   | ဗ္ဗ  | >              | CA   | X        |  |
| attegeggeegetegaecteagectegeagageegeetegeegegteetegeegegtegegeetegeegegtegeetegeege   | 9091     | gac  | GAG           | S  | GGT  | >   | CAG        | ß   | GGA       | 回  | ATG  | U        | GAT  | Σ   | GTA  | >1  | GAC  |     | CAA  | M              | GGA  | Ω        |  |
| attegegecgetegaceteagectegeagagecgegeteetacet tgegeteacetggeceagecetggecegagteegegeteacet tgegeteacetggeceagecetggecegagteegegectegeceg caatgtgeeggtectagetgaagateTCCGGGGTGTCTGAGC  | gcg      | agg  | CTI           | H  | GGT  | >   | CAN        | Z   | CCA       |    | TGA  | ы        | ACA  | ø   | GAG  | æ   | CAG  |     | CAG  | တ              | CAA  | ×        |  |
| attcgcggccgctcgacctcagcctcgaggcagagccgcgcgctctatggcgcacctggcccgggtccgagtccgagtccgagtccgcgcctcgccagtcagcccgggcccgagtccgcgcctcgccagtccacctggcccggagcccgagtccgagtccgagtccgagtccgagtccgagtccgagtccgagtccgagtccgagtccgaggcccagagtccgaggcccagagtccagagtccagagtccagagtcgaggccagagtcgaggcccagagcccagagcccagagcccagagcccagagcccagagcccagagcccagagcccaagagcccaagagcccaagagcccaagagcccaagagccagaaga  | cct      | SCG  | 000           | ρ, | GGI  | >   | 2          | ß   | GAT       | Н  | ပ္ပ  | 4        | S    | p,  | GTG  | 3   | AGA  |     | ည္ပည | æ              | CIL  | [kų      |  |
| attcgcggccgctcgacctcagcctgcaggcagagccgcgtc tgcgctcacctggcccagcccggagccctggcccgagtcggagcctgagagcctggccgagtcggcgcc caatgtgccggtcctagctgcagtctgagaggATGTCGGGGGTGTC   | cta      | cgo  | TGA           | 臼  | CAT  | Σ   | CIA        | ×   | AGA       | 回  | GCT  | Н        | GCA  | Ħ   | TGA  | 回   | AGA  | M   | CTA  | <b>&gt;</b> 1- | ATT  | Ŀ        |  |
| attegeggeegetegaecteageeteggeagageegegeetegeet  | gto      | cct  | GTC           | ß  | SS   | ρ,  | CTI        | Œ   | GAC       | H  | CCA  |          | GCT  | ı   | AGC  | 4   | GAA  | ×   | ACG  | CC;            | GAG  | æ        |  |
| attegeggeegetegaecteageetgeagageegtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegeagtegaggeetggeegagtegeagtegaggargategaggtectagetgagaggargategagtegeagtegaggargategaggtectagaggargategaggtectagaggargategaggargategagagategagagategagagagategagagagaga   | cgc      | gcg  | LDD           | >  | AGA  | 回   | CTG        | U   | GCA       | a  | CAT  | н        | CTG  | 3   | GGA  | 臼   | CCT  | н   | GCA  | a              | CAG  | æ        |  |
| attegeggeegetegaceteageetetgeaggeagag tgegeteacetggeeageetegagagargte CaatgtgeeggteetagetgeagtetgagaggATGTC V K V G T L R R P E G P CAGTGGATGTGGAGAGAGAGACGTGCCATCCTCAA V D V E K E D V R I L K TCAACCCAGGAAGAAGACTTGTCAAATGCAC N P G K N F K L V K C T TCATCACCTCCTCTGAGTGGCGCATTGCAC I T S I L S G R I G P ATGGGCTGAGGCTGAAGGATAGGGC  ATGGGCTGAGGCTGAAGTGAATGCAC  CCGTGGGCAAGAGCATAGGGC  A C C C C A C C C C A C C C C A C C C C  | CCG      | Itco | 990;          | U  | S    | Д   | GGT        | >   | AGT       | >  | CAA  | z        | CCA  | Ħ   | CGT  | >   | GAG  | ഗ   | CAT  | Σ              | GCT  | н        |  |
| attegeggeegetegaecteageetegeagea tgegeteacetggececegaegecetggececeagetegaegegar  caatgtgeeggtectagetgeagtetgagaggAT   | ıgag     | gag  | GTC           | ഗ  | ညည   | ρι  | CAS        | ×   | CAC       | H  | 009  | Ω,       | GAT  | Н   | ACA  | ш   | GGA  | ы   | CIA  | ×              | GGA  | ω        |  |
| attegeggeegetegaecteageetegeagetegeageteaget  | lgca     | Jaca | IgAI          | Σ  | 999  | U   | CCI        | Н   | ATG       | ပ  | AGG  | <b>U</b> | CGA  | 囮   | TCI  | Н   | CAT  |     | TGA  | Ω              | TCT  | Н        |  |
| attegeggeegetegacetege tgegeteacetggeceagecetege caatgtgeeggtectagetgeagtetga caatgtgeeggtectagetgeagtetga caatgtgeeggtectagetgeagtetga  V K V G T L R R P CAGTGGATGTGGAGAAGACGTGCG  V D V E K E D V R TCAACCCAGGGAAGAACTTCAAGCTTGT  N P G K N F K L V TCATCACCTCCATCCTCCTGAGTGGGCG  I T S I L L S G R ATGGGCTGAAGCACATGAAGTC  G L R L K H M K S CCGTGGCGAAGTGCAGGACAAGTATGA  V G E V Q D K Y E ACCTTCAAATCCGCTACTTGCCGGAAGA  L Q I R Y L P E D CATTGCTGTACTTTATCAACACCCGG  L L Y F Y Q O L R TCAGTGAAGGCATGGCTGGGG  S E G M A L Q L R TCAGTGAAGGCATGGCTCGGGA  TCAGTGAAGGCATGCTCTGCAGCTGGGG  CATTGCTGTACTTTATCAACACACGGGGGG  CATTGCTGTACTTTATCAACACACGGGGGGG  CATTGCTGTACTTTATCAACACACGGGGGGGG  TCAGTGAAGGCATGGCTCTGCAGCTGGGG  CATTGCTGTACTTTATCAACACACGCTGGGG  CATTGCTGTACTTTATCAACACACGCTGGGGGC  CATTGCTGTACTTTATCAACACACGCTGGGG  CATTGCTGAAGGCATGCCTCTGCAGCTGGGG  CA C C C C C C C C C C C C C C C C C C | Icag     | tgg  | ıgag          |    | TGA  |     | CAT        | Н   | CAA       | ×  | AAT  | н        | AGA  | Ω   | ATG  | ပ   | CTT  | [z. | GAA  | Z              | CTG  | ပ        |  |
| tgcgctcacctcgacctcagcct<br>tgcgctcacctggcccagccggag<br>caatgtgccggtcctagctgcagtc<br>V K V G T L R R<br>CAGTGGATGTGGAAGGAAGCGT<br>V D V E K E D V<br>TCAACCCAGGGAAGAAGCTTCAAGCT<br>I T S I L S G<br>ATGGGCTCATCCTCTGAGTGA<br>G L R H M K<br>CCGTGGCCGAAGTACAAGTA<br>V G E V Q D K Y<br>ACCTTCAAATCCGCTACTTGCGGA<br>L Q I R Y L P E<br>CATTGCTGTACTTTTATCAACAGCT<br>L Y F Y Q Q L<br>TCAGTGAAGGCATGGCTCTGCAGCT<br>S E G M A L Q L   | ctg      | CCC  | tga           |    | ည    |     | 909        | ĸ   | TGI       | >  | 909  |          | GTC  | ഗ   | TGA  | 臼   | AGA  | Ω   | SCCG | æ              | 999  | Ŋ        |  |
| attegeggeegetegaceteageteageteageteagete  | cct      | gag  | gto           |    | 900  | 8   | CGI        | >   | GCT       | Н  | TGG  | U        | GAA  | ×   | GTA  | ×   | GGA  | ы   | GCT  | н              | GCT  | н        |  |
| attegeggeegetegaect tgegeteacetggeecage caatgtgeeggtectaget V K V G T L CAGTGGATGTGGAAGGA V D V E K E TCAACCCAGGGAAGCA I T S I L L ATGGGCTGAGGCACTT G L R L K H G L R L K H CCGTGGGCTGAGGAGGA G L R L K H CCGTGGGCGAAGTGCAGGA  V G E V Q D ACCTTCAAATCCGCTACTT L Q I R Y L CATTGCTGTACTTTATCA L Y F Y Q TCAGGTGAAGGCACT  CATTGCTGTACTTTATCA L Y F Y Q TCAGTGAAGGCATGGCTCT  S E G M A L  | cag      | 500  | gca           |    | ACG  | oc, | AGA        | Ω   | CAA       |    | GAG  | ß        | CAT  | Σ   | CAA  | ×   | ၁၁၅  | ρ,  | ACA  | a              | GCA  | a        |  |
| attegeggeegetegategeegeaatgtgeegeegeteaatgtgeeggteeta  caatgtgeeggteeta  v k v G T  cagredargregaaa  v b v E K  rcaacccagggaaa  v b v E K  rcaacccaggaaaa  v b c K  rcaacccaggaaaa  i r s i L  argagcraaccrccarccr  carcaccagaagreeta  v G E v Q  accrrcaarccgcra  rcarcacrcaaccra  v G E v Q  accrrcaarccgcra  rcarcacrcaarccgcra  rcarcacrcaarccgcra  rcarraccrgracrrrrra  r v F Y  rcagraaaccarrcacc  s r A A  | cct      | ago  | gct           | ı  | TTT  | Н   | 35         | 臼   | CTI       |    | CCT  | Н        | GCA  | Ħ   | GGA  | Ω   | CII  |     | TCA  | a              | TCI  | н        |  |
| attegeggeeget tgegeteacetgg caatgtgeeggte V K V G CAGTGGATGTGGA V D V E TCAACCCAGGGAA N P G K TCATCACCTCCAT I T S I ATGGGCTGAGGCT G L R L CCGTGGGCTGAGGT V G E V ACCTTCAAATCCG L Q I R L Q I R CATTGCTGTAATCCG L Q I R CCGTGGGCGAAGT V G E V ACCTTCAAATCCG L Q I R CCGTGGGCTGAGGT CCGTGGGCGAAGT CCGTGGCTGAAGT CCGTGGGCGAAGT CCGTGGCTGAAGT CCGTGGCTGAAGT CCGTGGCTGAAGT CCGTGGCTGAAGT CCATTGCTGTAACTT CCATTGCTGTAACTT CATTGCTGTAAGGCAT  | cga:     | Jaco | cta           |    | CAC  | H   | GAR        | ×   | GAA       |    | CCT  | Н        | GAA  | M   | GCA  | ø   | CTA  | ×   | TTA  | ×              | SGC  | æ        |  |
| attegeggee tgegetcace caatgtgeeg  V K V V K V V D V CAGTGGATGT V D V TCAACCCAGG N P G TCATCACCTC I T S ATGGGCTGAG G L R G L R CCGTGGGCGAAT L Q I CATTGCTGTA L Q I CATTGCTGTA L Y TCAGTGAAGG S E G   | gct      | tgo  | gto           | )  | 000  | U   | ,GG2       | 凹   | GAA       |    | CAT  | Н        | GCT  | Н   | AGT  | >   | SCCG | ĸ   | CTT  | Ţ              | CAT  | X        |  |
| attegeg<br>tgegete<br>caatgtg<br>cagrega<br>v b<br>rcaacco<br>n P<br>rcaacco<br>g L<br>g L<br>ccgrege<br>v G<br>accrrca<br>L Q<br>carrecr<br>L D<br>rcagrega  | Igco     | acc  | ရီသည်<br>(၁၈) |    | AGI  | >   | TGI        | >   | AGG       | IJ | CTC  | ß        | GAG  | ×   | CGA  | 臼   | AAT  | Н   | GTA  | ×              | AGG  | <b>U</b> |  |
| tgeg<br>caat<br>caat<br>V CAGI<br>V TCAA<br>I ATGG<br>G CCGI<br>V ACCI<br>L CATI  | goba     | cto  | gtg           | )  | AAA  | ×   | <b>GGA</b> | Q   | SSS       | Д  | CAC  | H        | GCT  | H   | 999  | IJ  | TCA  | ø   | GCT  | н              | TGA  | 阳        |  |
|   | atto     | tgcg | caat          |    | GTGT | >   | CAGT       | >   | TCAA      | Z  | TCAT | н        | ATGG | U   | CCGT | >   | ACCT | н   | CATT | н              | TCAG | S        |  |

1020 1080 1140 1200 310 230 250 096 270 290 330 900 C) TGGACCTGTTTTCCCAAAGCAGATGCAGGAAAACTTAAAGCCCAAGCAGTTCCGGAAGA TGATCCAGCAGACCTTCCAGCAGTATGCATCACTCCGGGAGGAAGAGTGTGTCATGAAAT rgaccaggagacctaccgctgcgaactca **TTCAAGGATGGAACATTACTGTGGACCTGGTCATCGGCCCTAAAGGCATCCGTCAGCTGA** CAAGTCAAGATACAAAGCCCACCTGCCTGGCCGAGTTTAAGCAGATCAGATCCATCAGGT GCCTCCCATTGGAAGAGACCCAGGCAGTCCTGCAGCTGGGCATCGAGGGTGCCCCCAGT CCTTGTCTATCAAACGTCGTCCTGGCAGAGGCTGAGAACATGGCTGATCTCATAGATG GTGAGAAGAGGAACAGCCTGCCTCAGATCCCCACACTAAACCTGGAGGCTCGGCGGTCGC Δ U a S CGATGA æ X 闽 ρι M ഠ > U ĸ S 4 K O U Ω M ø, U 4 Æ, 4 囧 闰 U 回 H K 田 a Н × Н Σ Д E Σ 臼 Ы 闰 Н × 臼 × r Z 回 Д Z Н œ G 闰 Ø 14 Н 回 Ы H  $\Rightarrow$ CTGCAGCATAGAGTCAGACAT O 臼 Œ Z Ы Ω ď ഗ H 4 Н 臼 > 回 G Z S н S a K Н > 4 Z × ຜ × Σ ø a U 4 Ц ш Q 回 K O 0 H a ຜ > 臼 ρ, Ω × O U H ρ, H S U S Н  $\rho_4$ × H Н 臼 Ø S Н K Z H [4 H Ш Н × Z ഗ **[34** Ø H 3 Ω Z Н æ pc, 回 田 O Ç a Д Z S U S O S

|  |                |  |          | •  |        |  |     |  | •   | 3/6  | ,   |   |     |  |       |
|--|----------------|--|----------|--|--------|--|-----|--|-----|--|-----|---|-----|--|-------|
| 1440   | 430            | 1500   | 450      | 1560   | 470    | 1620   | 490 | 1680   | 510 | 1740   | 530 | 1800  | 550 | 1860                                       | 570   |
| GCA  | H              | 999  | E        | AGA  | ×      | TGA  | H   | AGC  | H   | ACA  | E   | ATA   | H   | 299  | 긔     |
| ည  | æ              | AG   | ប        | 9  | Œ      | CC   | Ţ   | GG   | Œ   | GT   | ¥   | 9   | Δ   | Ţ  | U     |
| TAA  | Z              | CAA  | ×        | CAA  | ×      | GAA  | M   | TGG  | ប   | CCT  | VL  | CAG   | R   | CTT  | E     |
| ្រួ  | ы              | ວິ   | B        | 3  | Z      | Ş  | >   | LT   | >   | 361  | >   | 35  | H   | Ş  |       |
| AGT  | Δ              | GAA(   | Z        | GGA  | Ω      | CAT(   | H   | TCC  | ы   | TCT(   | П   | TGT(  | Λ   | 955  | บ     |
| AGT  | Λ              | CAC  | Ŧ        | CCA  | a      | TCA  | H   | GTA  | ¥   | CAC  | Ŧ   | CTG   | ပ   | CCT  | 13    |
| AG2  | Œ              | CIP  | *        | LAC  | ī      | $\ddot{z}$                                   | ы   | ACI  | 1   | 300  | Д   | CAA   | Z   | SAA  | ×     |
| TCCACAGTACGGTGTTGCCCGTGAAGAAGTAGTTCTTAACCGCA | Œ              | CTTTGGGGAGGTCTATGAAGGTGTCTACACGAACCACAAAGGGG | >        | CGTCAAGACCTGTAAGAAAGACTGTACCCAGGACAACAAGGAGA | ပ      | AGTGATCATGAAGAATCTTGACCACCCTCACATCGTGAAGCTGA | H   | GGAACCCACCTGGATTATCATGGAACTGTATCCTTATGGGGAGC | ы   | <b>ACGAAATAAAAACTCCCTGAAGGTACCCCACTCTGGTCCTGTACA</b> | Δ   | <b>AGCCATGGCCTATCTGGAGGATCAACTGTGTGCACAGGGATA</b> | H   | CCTGGTGGCCTCTCCTGAGTGTGAAGCTGGGGGACTTTGGGC | Þ     |
| ၅၁၁  | R              | AGG  | ប        | AGA  | ۵      | TGA  | Q   | CAT  | X   | GAA  | X   | GAG   | S   | GTG  | ပ     |
| TGC  | A              | TGA  | E        | GAA  | X      | TCI  | Н   | TAT  | Ħ   | CCI  | I   | GGA   | ы   | TGA  | ω     |
| TGI  | >              | CTA  | ¥        | TAA  | X      | GAA  | Z   | GAT  | H   | CTC  | S   | TCI   | ы   | TCC  | a     |
| 9921   | U              | GGT  | ۸        | CTG  | ບ      | GAA  | X   | CTG  | M   | AAA  | Z   | CTA   | >   | CTC  | S     |
| GTA  | ×              | GGA  | Œ        | GAC  | Ŧ      | CAT  | Σ   | CAC  | T   | TAA  | ×   | 255   | Æ   | ၁၅၅  | A     |
| ACA  | ø              | TGG  | ប        | CAA  | K      | GAT  | H   | ACC  | Ъ   | AAA  | N   | CAT   | E   | GGT  | Þ     |
| TCC  | Δ,             | CTI  | Œ        | CGI  | ۸      |  | ۸   | GGA  | B   |  | ĸ   | AGC   | A   | CCT  | 긔     |
| AGG  | ŋ              | CTT  | ß        | 299  | Æ      | 299  | A   | AGA  | ы   | GGA  | ы   | CAA   | ×   | CAT  | н     |
| AGG  | <sub>U</sub>   | AGG  | U        | TGT  | Þ      | TGA  | 囟   | TGA  | ы   | LOO  | YL  | ATG   | ပ   | GAA  | Z     |
| ACC  | ρ <sub>4</sub> | TGA  | <b>E</b> | TAA  | Z<br>H | GAG  | S   | CAT  | II  | CTA  | ×   | GAT   | H   | SCG  |       |
| AAG  | æ              | 999  | ບ        | AAT  | Н      | CAT  | F   | CAT  |     | ACA  | G H | ACA   | a   | TGT  | A V R |
| TGCGAAGACCAGGAGG                             | æ              | TTCTGGGTGAAGGCTT                             | н        | AAAAATTAATGTGGC                              | ×      | AGTTCATGAGTGAGGC                             | E   | TTGGCATCATTGAAGA                             | ย   | TGGGACACTACCTGGA                                     | ีย  | CCCTACAGATATGCAA                                  | 17  | TTGCTGTCCGGAACAT                           | A     |
|  |                |  | <b>—</b> | 1~   | _      | 1~   |     | 15   |     | 15   |     | ı   |     | le.  | ۷     |

FIG. 1(

2760 2820 2880 2940 3000 850 870 890 930 GAGAAGAGGCCCAGCACCTCTGGGAGGAGGAGAAGATCAAGATGAAGCAGGTCCTAGAAA Gacagaagcagatggtggaagattcccagtggctgaggcgagggaaagatgcttgg K **ACCCTATGGTTTATATGAATGACAAGTCCCCACTGACTCCAGAGAAGGAGGCCGGCTACA** CAGCCAACCTGGACAGGACCGATGACCTCGTGTACCACAATGTCATGACCCTGGTGGAGG GCTGGAACTCAAGAACAAGCTTGGCCAGTTGCCCCTGAGGACTATGTGGTGGTGG TGGCAGAGCTCATCAACAAGATGAAGTTGGCTCAGCAGAACGCCGTGACGTCCTGAGTG 回 **AGGACTGCAAGCGGCAGATGCTCACAGCGTCCCATACCCTGGGTGTGGATGCCAAGAACC** TGCTGGATGCTGTGGACCAAGCTAGGTTGTGGCTAATCTGGCCCACCCGCCTGCAGAGt H U O > > H CCTTGCCGGCATCTTCGAGGACAGAGTTGAAGGGACCCAGAAACTGCTCAA CATCGGCAGTGTGGACGATCT 民 回 回 H S Q 山 K ø Σ Ω K Ω Н Σ æ > 回 国 > × K 叱 U Z Д O μ ഗ **H** H H 田 U Д O 3 Н ø Н U Q Ш × **GAAGA**ACGTGGGGCTGAACCTGCGGAAGCT ø Д > 闰 D, O Н K 回 ល ທ ທ H U K p, K Ω Ω 闰 × K Н (L) K H Ω 闰 0 × Σ П > Z Д H ĸ Z Z Д E Ø ĸ H K S Z 0 Q U Н U ഗ K 4 × H H Ø, Œ > O U X <u>[4</u> Z Z 回 回

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gatcaagagagggccacctgcctgcatcttctgcccccacctgtcttggcatacctttc ctgeettgeetttggttattggtettecagggaaagetgagaagagteeateeeettge cactttqcacqacacccctcttcccccaacccagccagactgtgctactcaggctgca ctactgccagccactccttaccccagcctgggttgctggagcatcattggggtcatg agtgtacccctaacggccaagatggctttctgcatggacatttgagagccagtattcctc cttcctcttcagccctcagggacccctgatacagaggggacagagaggggttttatttgt agagaagetggtgagatgagggetggaeetggetetettgtaeagtgtaeattggaattt atttaatgtgagtttgacctggatggacagccaagggccatagtccaggagcaaaccaat ccagtcacaggactctgtgttttatggaactgagtgccacaggaagaagcagagtcgg **ettttettacgteteettttteteeteeeetttteacatetgeteeeetetetet** gtctgtggagaacatttaccttccttcttttgatcggtggttgaattaaaattattacc atttgctttgtggctcgtgcc

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## INTERNATIONAL SEARCH REPORT

International application No. PCT/US98/02494

| A. CLASS               | SIFICATION OF SUBJECT MATTER   |  |                                  |
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|                        | 12N 1/00, 5/10, 15/54; C12Q 1/48, 1/68   | •  |                                  |
|                        | 536/23.2; 435/6, 252.3, 254.11, 325, 410   |  | i                                |
| According to           | International Patent Classification (IPC) or to both nat   | ional classification and IPC   |                                  |
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| Minimum doc            | cumentation scarched (classification system followed by  | classification symbols)  |                                  |
| U.S. : 5               | 36/23.2; 435/4, 6, 7.4, 15, 194. 252.3, 254.11, 320.:  | 1, 325, 410  |                                  |
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| Documentatio           | n searched other than minimum documentation to the ext   | ent that such documents are included   | in the fields searched           |
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| Electronic dat         | ta base consulted during the international search (name  | of data base and, where practicabl   | c, scarch terms used)            |
| Please See             | Extra Sheet.   |  |                                  |
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| C. DOCU                | MENTS CONSIDERED TO BE RELEVANT  |  |                                  |
| Category*              | Citation of document, with indication, where appro   | priate, of the relevant passages   | Relevant to claim No.            |
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| Purthe                 | r documents are listed in the continuation of Box C.   | See patent family annex.   |                                  |
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| Receimile No.          | (703) 305-3230   | mhone No. (703) 308-0106   | ,                                |

## INTERNATIONAL SEARCH REPORT

International application No. PCT/US98/02494

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